

**FIG. 1**

CGGGGGGATAACCCCAAGGAGATGGGGTCGAGGAGACCCCCGGGAGTAGAGAGAAACTCACTC	71
CCCGAGTCCCCGACCCCTCCCCAAGCAAGGTATAATA <u>AAC</u> TATCCTCATGGCTTTCCCTGCCCTT	142
CTCCCCAATCATCAACAATAGAAGAAAGAACATG TCA GGA CAC AAA TGC AGT TAT CCC	205
Met Ser Gly His Lys Cys Ser Tyr Pro	9
 TGG GAC TTA CAG GAT CGA TAT GCT CAA GAT AAG TCA GTT GIA AAT AAG ATG CAA	259
Trp Asp Leu Gln Asp Arg Tyr Ala Gln Asp Lys Ser Val Val Asn Lys Met Gln	27
CAG AGA TAT TGG GAG ACG AAG CAG GCC TTT ATT AAA GCC ACA GGG AAG AAG GAA	313
Gln Arg Tyr Trp Glu Thr Lys Gln Ala Phe Ile Lys Ala Thr Gly Lys Lys Glu	45
GAT GAA CAT GTT GCC TCT GAC GCG GAC CTG GAT GCC AAG CTA GAG CTG TTT	367
Asp Glu His Val Val Ala Ser Asp Ala Asp Leu Asp Ala Lys Leu Glu Leu Phe	63
CAT TCA ATT CAG AGA ACC TGT CTG GAC TTA TCG AAA GCA ATT GTA CTC TAT CAA	421
His Ser Ile Gln Arg Thr Cys Leu Asp Leu Ser Lys Ala Ile Val Leu Tyr Gln	81
CK2	
AAG AGG ATA TGT TTC TTG TCT CAA GAA AAC GAA CTG GGA AAA TTT CTT CGA	475
Lys Arg Ile Cys Phe Leu Ser Gln Glu Glu Asn Glu Leu Gly Lys Phe Leu Arg	99
TCC CAA GGT TTC CAA GAT AAA ACC AGA GCA GGA AAG ATG ATG CAA GCG ACA GGA	529
Ser Gln Gly Phe Gln Asp Lys Thr Arg Ala Gly Lys Met Met Gln Ala Leu Arg Asn Pro Leu Cys	135
CGA TTT CAC CAA GAA GTG GAG ACT TTT CGG CAT CGG GCC ATC TCA GAT ACT TGG	637
Arg Phe His Gln Glu Val Glu Thr Phe Arg His Arg Ala Ile Ser Asp Thr Trp	153
CTG ACG GTG AAC CGC ATG GAA CAG TGC AGG ACG GAA TAT AGA GGA GCA CTA TTA	691
Leu Thr Val Asn Arg Met Glu Gln Cys Arg Thr Glu Tyr Arg Gly Ala Leu Leu	171

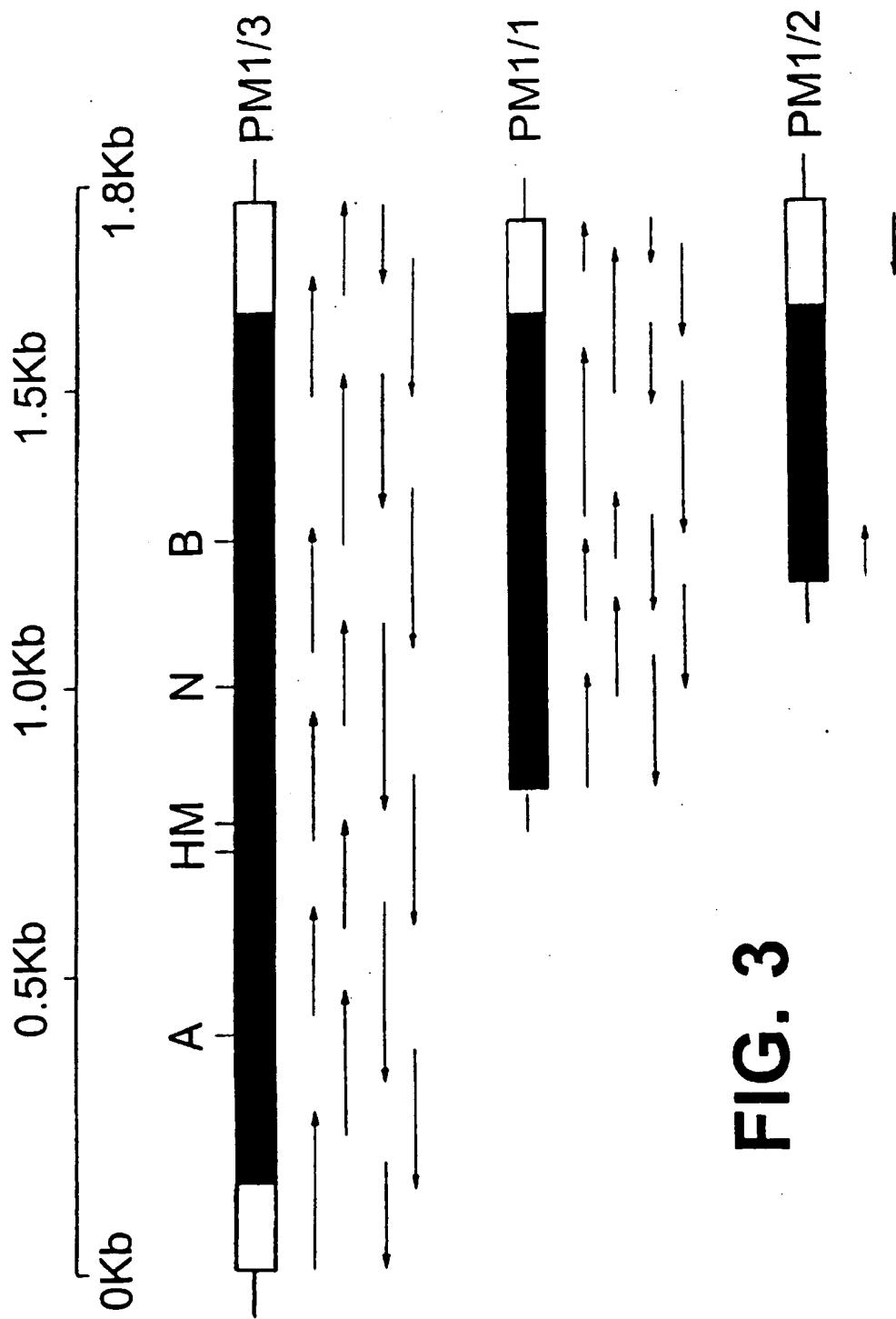
**FIG. 2A**

TGG	ATG	AAG	GAC	GTG	TCT	CAG	GAG	CTT	GAT	CCA	GAC	CTC	TAC	AAG	CAA	ATG	GAG	745
Trp	Met	Lys	Asp	Val	Ser	Gln	Glu	Leu	Asp	Pro	Asp	Leu	Tyr	Lys	Gln	Met	Glu	189
AAG	TTC	AGG	AAG	GTG	CAA	ACA	CAA	GTG	CGC	CTT	GCA	AAA	AAA	AAC	TTT	GAC	AAA	799
Lys	Phe	Arg	Lys	Val	Gln	Thr	Gln	Val	Arg	Leu	Ala	Lys	Lys	Asn	Phe	Asp	Lys	207
RTG	AAG	ATG	GAT	GTG	TGT	CAA	AAA	GTG	GAT	CTT	CTT	GGA	GCG	AGC	AGA	TGC	AAT	853
Leu	Lys	Met	Asp	Val	CYS	Gln	Lys	Val	Asp	Leu	Leu	Gly	Ala	Ser	Arg	Cys	Asn	225
CTC	TTG	TCT	CAC	ATG	CTA	GCA	ACA	TAC	CAG	ACC	ACT	CTG	CTT	CAT	TTT	TGG	GAG	907
Leu	Leu	Ser	His	Met	Leu	Ala	Thr	Tyr	Gln	Thr	Thr	Leu	Leu	His	Phe	Trp	Glu	243
AAA	ACT	TCT	CAC	ACT	ATG	GCA	GCC	ATC	CAT	GAG	AGT	TTC	AAA	GGT	TAT	CNA	CCA	961
Lys	Thr	Ser	His	Thr	Met	Ala	Ala	Ile	His	Glu	Ser	Phe	Lys	Gly	Tyr	Gln	Pro	261
TAT	GAA	TTT	ACT	ACT	TTA	AAG	AGC	TTA	CAA	GAC	CCT	ATG	AAA	AAA	TTA	GTT	GAG	1015
Tyr	Glu	Phe	Thr	Thr	Leu	Lys	Ser	Leu	Gln	Asp	Pro	Met	Lys	Lys	Leu	Val	Glu	279
AAA	GAA	GAG	AAG	AAA	ATC	AAC	CAG	CAG	GAA	AGT	ACA	GAT	GCA	GCC	GTG	CAG	1069	
Lys	Glu	Glu	Lys	Lys	Ile	Asn	Gln	Gln	Glu	Ser	Thr	Asp	Ala	Ala	Val	Gln	297	
												AMP						
GAG	CCG	AGC	CAA	TTA	ATT	TCA	TTA	GAG	GAA	AAC	CAG	CGC	AAG	GAA	TCC	TCT		1123
Glut	Pro	Ser	Gln	Leu	Ile	Ser	Leu	Glu	Glu	Asn	Gln	Arg	Lys	Glu	Ser	Ser		315
PKC												CK2						
AGT	TTT	AAG	ACT	GAA	GAT	GGA	AAA	AGT	ATT	TTA	TCT	GCC	TTA	GAC	AAA	GGC	TCT	1177
Ser	Phe	Lys	Thr	Glu	Asp	Gly	Lys	Ser	Ile	Leu	Ser	Ala	Leu	Asp	Lys	Gly	Ser	333
ACA	CAT	ACT	GCA	TGC	TCA	GGG	CCC	ATA	GAT	GAA	CTA	TTA	GAC	ATG	AAA	TCT	GAG	1231
Thr	His	Thr	Ala	Cys	Ser	Gly	Pro	Ile	Asp	Glu	Leu	Asp	Met	Lys	Ser	Glu	351	

**FIG. 2B**

GAA	GGT	GCT	TGC	CTG	GGA	CCA	GTG	GCA	GGG	ACC	CCG	GAA	CCT	GAA	GGT	GCT	GAC	1285	
Glu	Gly	Ala	Cys	Leu	Gly	Pro	Val	Ala	Gly	Thr	Pro	Glu	Pro	Glu	Gly	Ala	Asp	369	
						*											CK2		
AAA	GAT	GAC	CTG	CTG	CTG	TTG	AGT	GAG	ATC	TTC	AAT	GCT	TCC	TCC	TTG	GAA	GAG	1339	
Lys	Asp	Asp	Leu	Leu	Leu													Leu	387
GGC	GAG	TTC	AGC	AAA	GAG	TGG	GCC	GCT	GTG	TTT	GGA	GAC	GGC	CAA	GTG	AAG	GAG	1393	
Gly	Glu	Phe	Ser	Lys	Glu	Trp	Ala	Ala	Val	Phe	Gly	Asp	Gly	Gln	Val	Lys	Glu	405	
CCA	GTG	CCC	ACT	ATG	GCC	CTG	GGA	GAG	CCA	GAC	CCC	AAG	GCC	CAG	ACA	GCC	TCA	1447	
Pro	Val	Pro	Thr	Met	Ala	Leu	Gly	Glu	Pro	Asp	Pro	Lys	Ala	Gln	Thr	Gly	Ser	423	
																	CK2		
GGT	TTC	CTT	CCT	TCG	CAG	CTT	TTA	GAC	CAA	AAT	ATG	AAA	GAC	TTA	CAG	GCC	TCG	1501	
Gly	Phe	Leu	Pro	Ser	Gln	Leu	Leu	Asp	Gln	Asn	Met	Lys	Asp	Leu	Gln	Ala	Ser	441	
CTA	CAA	GAA	CCT	GCT	AAG	GCT	GCC	TCA	GAC	CTG	ACT	GCC	TGG	TTC	AGC	CTC	TTC	1555	
Leu	Gln	Glu	Pro	Ala	Lys	Ala	Ala	Ser	Asp	Leu	Thr	Ala	Trp	Phe	Ser	Leu	Phe	459	
GCT	GAC	CTC	GAC	CCA	CTC	TCA	AAT	CCT	GAT	GCT	GTG	GGG	AAA	ACC	GAT	AAA	GAA	1609	
Ala	Asp	Leu	Asp	Pro	Leu	Ser	Asn	Pro	Asp	Ala	Val	Gly	Lys	Thr	Asp	Lys	Glu	477	
CAC	GAA	TTG	CTC	AAT	GCA	TGA	ATCTG	TAC	CC	TT	GG	AGGG	CA	CT	AC	AT	GCC	1674	
His	Glu	Leu	Leu	Asn	Ala	END													
CCCCCTGGGGCTAGGCAGAAGTATAAAGTGATCAGTATGCTGTTAATTATGTCCTTTAATAATAAAAAAA																		1745	
TGAAGGGTCAACGGCCCTGTTAAAAAA																		1785	
																		483	

**FIG. 2C**



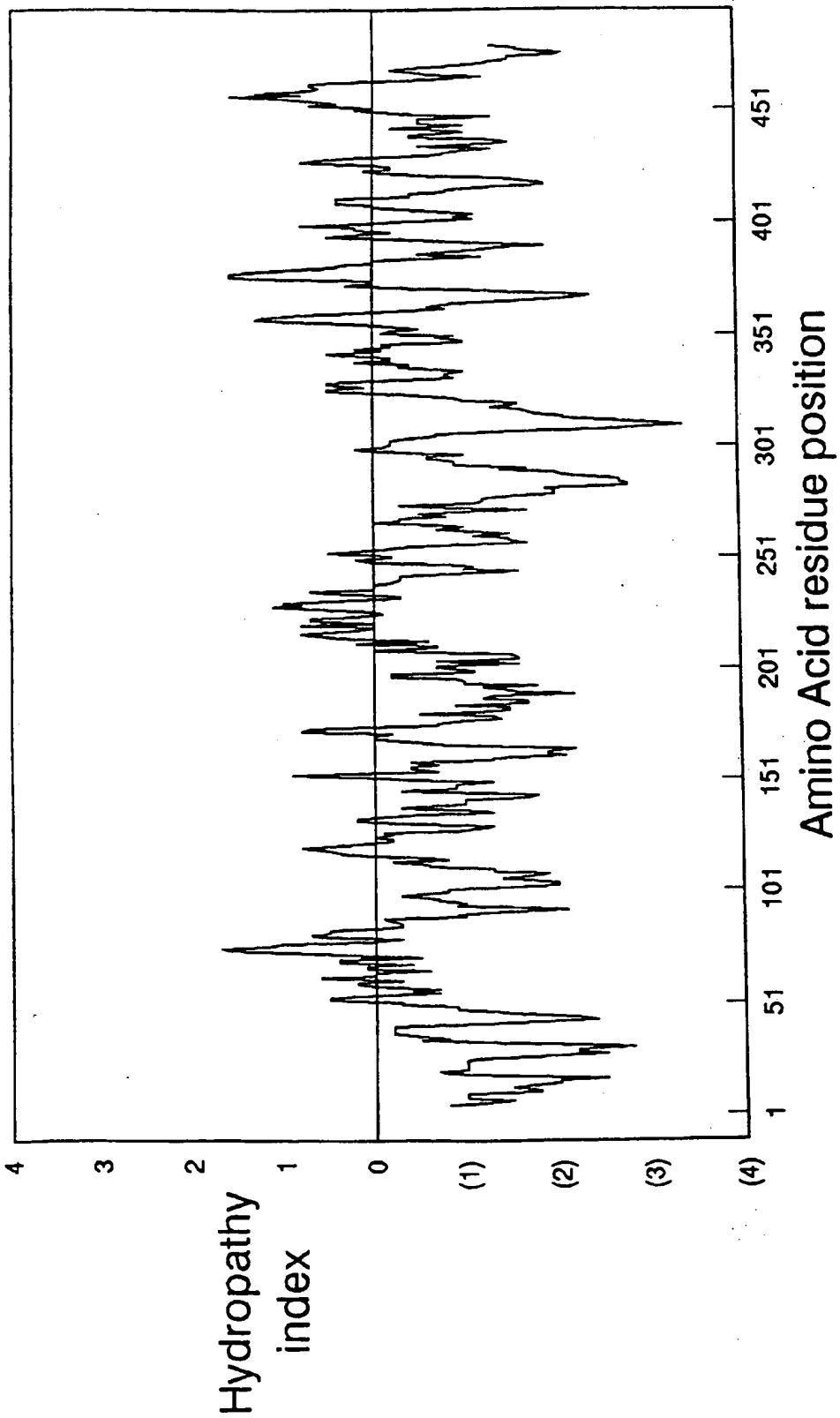
**FIG. 3**

N	F D K L K	M D	V	C	PM-1	205
V	F D K L K	H L	V	D	BSA	373

S	E	E	G A C L	G P	V	PM-1	351
*							
E	D	K	G A C L	L P	K	BSA	172

**FIG. 4**

**PM-1 Kyte and Doolittle Hydropathy Analysis**



**FIG. 5**

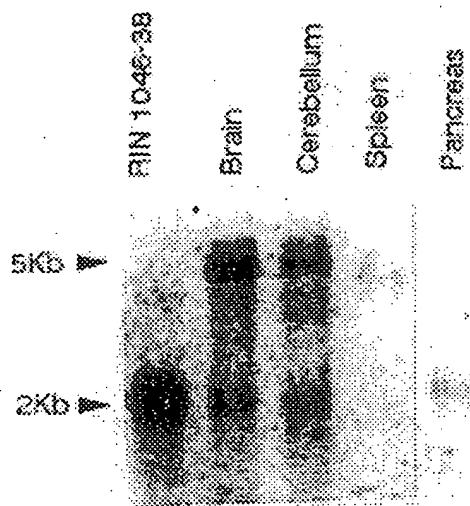


FIG. 6

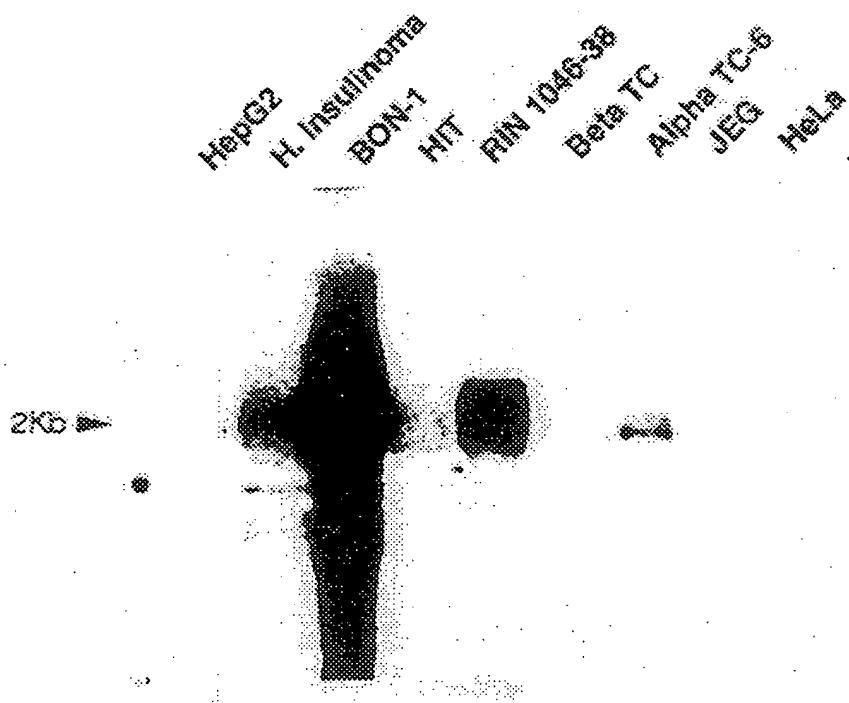


FIG. 7

